Raw Sequence Listing Error Summary

| ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/689,343_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _✓_ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _4_____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _✓_ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

File Copy

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH
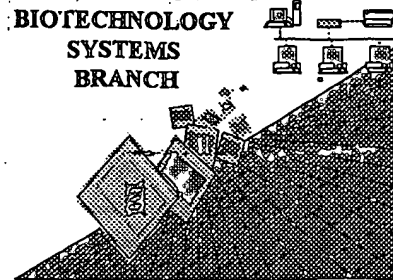
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/689,343

Source: OIPE

Date Processed by STIC: 10/27/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

RAW SEQUENCE LISTING   DATE: 10/27/2000
PATENT APPLICATION: US/09/689,343   TIME: 08:36:04

Input Set : A:\Neb-181.app
Output Set: N:\CRF3\10272000\I689343.raw

```
 3 <110> APPLICANT: VAISVILA, ROMUALDAS
 4         MORGAN, RICHARD D.
 5         KUCERA, REBECCA B.
 6         CLAUS, TOBY E.
 7         RALEIGH, ELISABETH A.
 9 <120> TITLE OF INVENTION: METHOD FOR CLONING AND PRODUCING THE MseI RESTRICTION
10         ENDONUCLEASE
12 <130> FILE REFERENCE: NEB-181
14 <140> CURRENT APPLICATION NUMBER: US/09/689,343
15 <141> CURRENT FILING DATE: 2000-10-12
17 <160> NUMBER OF SEQ ID NOS: 9
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 903
23 <212> TYPE: DNA
24 <213> ORGANISM: Micrococcus sp.
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(900)
30 <400> SEQUENCE: 1
31 atg cct atc tcg acc gtc tgg acg ccg gac gga gac gac ctc atc gtg    48
32 Met Pro Ile Ser Thr Val Trp Thr Pro Asp Gly Asp Asp Leu Ile Val
33  1               5                  10                  15
35 gag gcg gac aac ctc gat ttc att caa acg ctc ccc gac gcg agc ttc    96
36 Glu Ala Asp Asn Leu Asp Phe Ile Gln Thr Leu Pro Asp Ala Ser Phe
37              20                  25                  30
39 cga atg atc tac atc gat ccg ccg ttc aac aca ggg cga acg cag cgg   144
40 Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
41          35                  40                  45
43 ctt cag tcg ctc aag acg acc cgc tcg gtc aca ggg tcg cga gtc ggc   192
44 Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
45       50                  55                  60
47 ttc aaa ggc cag acg tac gac acg gtc aag agc act ctg cac tcg tat   240
48 Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
49 65                  70                  75                  80
51 gac gac gct ttc acc gac tat tgg tcg ttc ctc gaa ccg cgt ctc ctg   288
52 Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
53                  85                  90                  95
55 gag gct tgg cgg ttg ctc acc cct gac ggc gcg ctc tat ctt cat ctg   336
56 Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu
57              100                 105                 110
59 gat tac cgc gag gtt cac tac gcc aag gtc gtc ctc gac gcg atg ttc   384
60 Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe
61          115                 120                 125
63 gga cgc gaa agc ttc ctg aac gag ctg atc tgg gcg tac gac tac ggc   432
64 Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly
65          130                 135                 140
```

```
                  RAW SEQUENCE LISTING              DATE: 10/27/2000
                  PATENT APPLICATION:  US/09/689,343    TIME: 08:36:04

                  Input Set : A:\Neb-181.app
                  Output Set: N:\CRF3\10272000\I689343.raw

 67 gcg cgc tcg aag agc aag tgg ccc acc aag cac gac aac atc ctc gtg    480
 68 Ala Arg Ser Lys Ser Lys Trp Pro Thr Lys His Asp Asn Ile Leu Val
 69 145             150                 155                 160
 71 tat gtg aag gac ccg aac aac tac gtc tgg aac ggt cag gat gta gat    528
 72 Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp
 73                 165                 170                 175
 75 cgc gag ccc tac atg gcg ccc ggg ctc gtt aca ccc gag aag gta gcg    576
 76 Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala
 77                 180                 185                 190
 79 ctt ggc aag ctg ccc acc gac gtc tgg tgg cac aca atc gtt ccg cct    624
 80 Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro
 81         195         .           200                 205
 83 gcg agc aaa gag cgc acc ggg tac gcg aca cag aag ccg gtc ggc atc    672
 84 Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile
 85         210                 215                 220
 87 atc cgt cgc atg att cag gcg agc agc aat gaa ggc gac tgg gtt ctg    720
 88 Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu
 89 225                 230                 235                 240
 91 gat ttc ttc gct ggt agt ggg acg acc ggc gcc gcg gcc cgc cag ctc    768
 92 Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu
 93                 245                 250                 255
 95 gga cgc cgt ttt gtg ctc gta gac gtc aac cca gaa gca atc gcg gta    816
 96 Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val
 97                 260                 265                 270
 99 atg gca aaa cgg ttg gat gac ggg gca ttg gac acc agc gtg acg atc    864
100 Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile
101         275                 280                 285
103 gtg cag act ccc cag agt gac cca cga acc gac gga tga               903
104 Val Gln Thr Pro Gln Ser Asp Pro Arg Thr Asp Gly
105         290                 295                 300
108 <210> SEQ ID NO: 2
109 <211> LENGTH: 300
110 <212> TYPE: PRT
111 <213> ORGANISM: Micrococcus sp.
113 <400> SEQUENCE: 2
114 Met Pro Ile Ser Thr Val Trp Thr Pro Asp Gly Asp Asp Leu Ile Val
115   1               5                   10                  15
117 Glu Ala Asp Asn Leu Asp Phe Ile Gln Thr Leu Pro Asp Ala Ser Phe
118                 20                  25                  30
120 Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
121         35                  40                  45
123 Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
124         50                  55                  60
126 Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
127  65                  70                  75                  80
129 Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
130                 85                  90                  95
132 Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu
133         100                 105                 110
```

RAW SEQUENCE LISTING   DATE: 10/27/2000
PATENT APPLICATION: US/09/689,343   TIME: 08:36:04

Input Set : A:\Neb-181.app
Output Set: N:\CRF3\10272000\I689343.raw

```
135 Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe
136         115                 120                 125
138 Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly
139         130                 135                 140
141 Ala Arg Ser Lys Ser Lys Trp Pro Thr Lys His Asp Asn Ile Leu Val
142 145                 150                 155                 160
144 Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp
145                 165                 170                 175
147 Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala
148         180                 185                 190
150 Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro
151         195                 200                 205
153 Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile
154         210                 215                 220
156 Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu
157 225                 230                 235                 240
159 Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu
160                 245                 250                 255
162 Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val
163                 260                 265                 270
165 Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile
166         275                 280                 285
168 Val Gln Thr Pro Gln Ser Asp Pro Arg Thr Asp Gly
169         290                 295                 300
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 1236
174 <212> TYPE: DNA
175 <213> ORGANISM: Unknown
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Description of Unknown Organism: ENVIRONMENTAL DNA
180 <220> FEATURE:
181 <221> NAME/KEY: CDS
182 <222> LOCATION: (1)..(1233)
184 <400> SEQUENCE: 3
185 atg cct aca ctg gat tgg ccc ggt aaa cag tta agc ttc cca cca gct     48
186 Met Pro Thr Leu Asp Trp Pro Gly Lys Gln Leu Ser Phe Pro Pro Ala
187  1               5                  10                  15
189 acc tcc ttg cat ctg gag agt gtg gtc act gag gga gcg gag tca ccg     96
190 Thr Ser Leu His Leu Glu Ser Val Val Thr Glu Gly Ala Glu Ser Pro
191             20                  25                  30
193 cct aat cgt ctg att tgg gcg gac aac ctg ccg cta atg gta gat ttg    144
194 Pro Asn Arg Leu Ile Trp Ala Asp Asn Leu Pro Leu Met Val Asp Leu
195         35                  40                  45
197 ttg gcc gaa tat gaa ggg aaa atc gat ctg atc tac gcc gat ccc cct    192
198 Leu Ala Glu Tyr Glu Gly Lys Ile Asp Leu Ile Tyr Ala Asp Pro Pro
199         50                  55                  60
201 ttt ttt acg gat cgt act tat gcg gcg cga att ggt cat ggg gag gat    240
202 Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp
203 65                  70                  75                  80
```

```
                    RAW SEQUENCE LISTING                    DATE: 10/27/2000
                    PATENT APPLICATION:  US/09/689,343      TIME: 08:36:04

                    Input Set : A:\Neb-181.app
                    Output Set: N:\CRF3\10272000\I689343.raw

        205 tcg cgt cgt cca caa acc tgg cag ctt gca gaa gga tat acg gac gag   288
        206 Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu
        207              85                  90                  95
        209 tgg aag gat tta gat gaa tac ctg gac ttc ctt tat cca cgc ctg gta   336
        210 Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val
        211             100                 105                 110
        213 ctg atg tat cga ctg ctg gca cca cac gga acg ctc tac ttg cac ctg   384
        214 Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu
        215             115                 120                 125
        217 gac tgg cac gcc aat gcc tac gta cgt gta ctg ctt gat gag atc ttc   432
        218 Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe
        219         130                 135                 140
        221 ggg cga cag cgg ttt ctc aac gag atc gtc tgg atc tat cac ggc ccc   480
        222 Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro
        223 145                 150                 155                 160
        225 tca gcc atc cga cgc gcc ttc aag cgc aaa cat gat acc atc ttg gtt   528
        226 Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val
        227             165                 170                 175
        229 tat gtg aaa ggt gaa aac tat aca ttc aat gcg gat gcg gtt cgt caa   576
        230 Tyr Val Lys Gly Glu Asn Tyr Thr Phe Asn Ala Asp Ala Val Arg Gln
        231             180                 185                 190
W-->    233 cct tac cat ccg agc acn cat aag acc ttc gct tcc tcc ccg aag gcc   624
W-->    234 Pro Tyr His Pro Ser Xaa His Lys Thr Phe Ala Ser Ser Pro Lys Ala
        235             195                 200                 205
        237 ggc ttt ggt aag gtg ccg gat ctg cag cgc ggc aaa gtg ccc gaa gac   672
        238 Gly Phe Gly Lys Val Pro Asp Leu Gln Arg Gly Lys Val Pro Glu Asp
        239     210                 215                 220
        241 tgg tgg tat ttt ccg gtc gtg gcc cgt cta cac cga gaa cgg agc ggc   720
        242 Trp Trp Tyr Phe Pro Val Val Ala Arg Leu His Arg Glu Arg Ser Gly
        243 225                 230                 235                 240
        245 tat ccg act caa aag cct caa gcc ttg ctg gag cgg atc ctg ctg gcc   768
        246 Tyr Pro Thr Gln Lys Pro Gln Ala Leu Leu Glu Arg Ile Leu Leu Ala
        247                 245                 250                 255
        249 tcc tcg aac gca ggc gat ctg gtg gca gac ttc ttc tgc ggc tca ggg   816
        250 Ser Ser Asn Ala Gly Asp Leu Val Ala Asp Phe Phe Cys Gly Ser Gly
        251             260                 265                 270
        253 aca acc gct gtg gtg gca gcc cgt ctg gga cgg cgc ttc ctg gtc aac   864
        254 Thr Thr Ala Val Val Ala Ala Arg Leu Gly Arg Arg Phe Leu Val Asn
        255     275                 280                 285
        257 gat gca agc tgg cgc gcc gtt cat gtg aca cgc aca cgc ttg cta cgc   912
        258 Asp Ala Ser Trp Arg Ala Val His Val Thr Arg Thr Arg Leu Leu Arg
        259     290                 295                 300
        261 gag gga gta agt ttc act ttt gaa cgc cag gaa act ttt act cta cct   960
        262 Glu Gly Val Ser Phe Thr Phe Glu Arg Gln Glu Thr Phe Thr Leu Pro
        263 305                 310                 315                 320
        265 atc cag cca ctt cca cca gat tgg ttg atc atc gcc gag gag cag att  1008
        266 Ile Gln Pro Leu Pro Pro Asp Trp Leu Ile Ile Ala Glu Glu Gln Ile
        267                 325                 330                 335
        269 cgc ctc caa gca ccc ttt ctc gta gat ttt tgg gaa gtg gac gat caa  1056
```

→ see item 10 on Error Summary Sheet

```
270 Arg Leu Gln Ala Pro Phe Leu Val Asp Phe Trp Glu Val Asp Asp Gln
271             340             345             350
273 tgg gat ggc aaa atc ttc cgc agc cgt cat caa ggc tta cgc tcc cgc   1104
274 Trp Asp Gly Lys Ile Phe Arg Ser Arg His Gln Gly Leu Arg Ser Arg
275             355             360             365
277 ctt cag gag cag gcg ccg ctc tct cta cca ttg acc ggg aat gga ctg   1152
278 Leu Gln Glu Gln Ala Pro Leu Ser Leu Pro Leu Thr Gly Asn Gly Leu
279         370             375             380
281 ttg tgt gta cgg gta gtg agc cgt gaa ggg gaa tac tat gag ttc aca   1200
282 Leu Cys Val Arg Val Val Ser Arg Glu Gly Glu Tyr Tyr Glu Phe Thr
283 385                 390             395             400
285 ggt cga gcc gat agc cct cac ccc gta tcg ttt tga                    1236
286 Gly Arg Ala Asp Ser Pro His Pro Val Ser Phe
287             405             410
290 <210> SEQ ID NO: 4
291 <211> LENGTH: 411
292 <212> TYPE: PRT
293 <213> ORGANISM: Unknown
W--> 295 <220> FEATURE:
W--> 295 <223> OTHER INFORMATION:
295 <400> SEQUENCE: 4
296 Met Pro Thr Leu Asp Trp Pro Gly Lys Gln Leu Ser Phe Pro Pro Ala
297 1               5               10              15
299 Thr Ser Leu His Leu Glu Ser Val Val Thr Glu Gly Ala Glu Ser Pro
300             20              25              30
302 Pro Asn Arg Leu Ile Trp Ala Asp Asn Leu Pro Leu Met Val Asp Leu
303         35              40              45
305 Leu Ala Glu Tyr Glu Gly Lys Ile Asp Leu Ile Tyr Ala Asp Pro Pro
306         50              55              60
308 Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp
309 65              70              75              80
311 Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu
312             85              90              95
314 Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val
315             100             105             110
317 Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu
318         115             120             125
320 Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe
321         130             135             140
323 Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro
324 145             150             155             160
326 Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val
327             165             170             175
329 Tyr Val Lys Gly Glu Asn Tyr Thr Phe Asn Ala Asp Ala Val Arg Gln
330             180             185             190
W--> 332 Pro Tyr His Pro Ser Xaa His Lys Thr Phe Ala Ser Ser Pro Lys Ala
333             195             200             205
335 Gly Phe Gly Lys Val Pro Asp Leu Gln Arg Gly Lys Val Pro Glu Asp
336         210             215             220
```

see item 7 on Eva Summary Sheet

see item 10 on Eva Summary Sheet

VERIFICATION SUMMARY   DATE: 10/27/2000
PATENT APPLICATION: US/09/689,343   TIME: 08:36:05

Input Set : **A:\Neb-181.app**
Output Set: **N:\CRF3\10272000\I689343.raw**

L:14 M:270 C: Current Application Number differs, Replaced Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:295 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:295 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:332 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:332 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:332 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:474 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:474 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: